

FIGURE 1

1 GAACCAGCCT GCACGCGCTG GCTCCGGGTG ACAGCCGCGC GCCTCGGCCA
 51 GGATCTGAGT GATGAGACGT GTCCCCACTG AGGTGCCCCA CAGCAGCAGG
 101 TGTTGAGCAT GGGCTGAGAA GCTGGACCGG CACCAAAGGG CTGGCAGAAA
 151 TGGGCGCCTG GCTGATTCTT AGGCAGTTGG CGGCAGCAAG GAGGAGAGGC
 201 CGCAGCTTCT GGAGCAGAGC CGAGACGAAG CAGTTCTGGA GTGCCTGAAC
 251 GGCCCCCTGA GCCCTACCCG CCTGGCCAC TATGGTCCAG AGGCTGTGGG
 301 TGAGCCGCCT GCTGCGGCAC CGGAAAGCCC AGCTCTTGCT GGTCAACCTG
 351 CTAACCTTTG GCCTGGAGGT GTGTTTGGCC GCAGGCATCA CCTATGTGCC
 401 GCCTCTGCTG CTGGAAGTGG GGGTAGAGGA GAAGTTCATG ACCATGGTGC
 451 TGGGCATTGG TCCAGTGCTG GGCCTGGTCT GTGTCCCGCT CCTAGGCTCA
 501 GCCAGTGACC ACTGGCGTGG ACGCTATGGC CGCCGCCGGC CCTTCATCTG
 551 GGCAGTGTCC TTGGGCATCC TGCTGAGCCT CTTTCTCATC CCAAGGGCCG
 601 GCTGGCTAGC AGGGCTGCTG TGCCCGGATC CCAGGCCCCCT GGAGCTGGCA
 651 CTGCTCATCC TGGGCGTGGG GCTGCTGGAC TTCTGTGGCC AGGTGTGCTT
 701 CACTCCACTG GAGGCCCTGC TCTCTGACCT CTTCCGGGAC CCGGACCACT
 751 GTCGCCAGGC CTACTCTGTC TATGCCTTCA TGATCAGTCT TGGGGGCTGC
 801 CTGGGCTACC TCCTGCCTGC CATTGACTGG GACACCAGTG CCCTGGCCCC
 851 CTACCTGGGC ACCCAGGAGG AGTGCCTCTT TGGCCTGCTC ACCCTCATCT
 901 TCCTCACCTG CGTAGCAGCC AACTGCTGG TGGCTGAGGA GGCAGCGCTG
 951 GGCCCCACCG AGCCAGCAGA AGGGCTGTCT GCCCCCTCCT TGTCGCCCCA
 1001 CTGCTGTCCA TGCCGGGCCC GCTTGGCTTT CCGGAACCTG GGCGCCCTGC
 1051 TTCCCCGGCT GCACCAGCTG TGCTGCCGCA TGCCCCGCAC CCTGCGCCGG
 1101 CTCTTCGTGG CTGAGCTGTG CAGCTGGATG GCACTCATGA CCTTCACGCT
 1151 GTTTTACACG GATTTCGTGG GCGAGGGGCT GTACCAGGGC GTGCCCAGAG
 1201 CTGAGCCGGG CACCGAGGCC CGGAGACACT ATGATGAAGG CGTTCGGATG
 1251 GGCAGCCTGG GGCTGTTCTT GCAGTGCGCC ATCTCCCTGG TCTTCTCTCT
 1301 GGTCATGGAC CGGCTGGTGC AGCGATTCGG CACTCGAGCA GTCTATTGGA
 1351 CCAGTGTGGC AGCTTTCCCT GTGGCTGCCG GTGCCACATG CCTGTCCCAC
 1401 AGTGTGGCCG TGGTGACAGC TTCAGCCGCC CTCACCGGGT TCACCTTCTC

FIGURE 1 – continued

1451 AGCCCTGCAG ATCCTGCCCT ACACACTGGC CTCCTCTAC CACCGGGAGA
 1501 AGCAGGTGTT CCTGCCCCAA TACCGAGGGG ACACTGGAGG TGCTAGCAGT
 1551 GAGGACAGCC TGATGACCAG CTTCTGCCA GGCCCTAAGC CTGGAGCTCC
 1601 CTTCCCTAAT GGACACGTGG GTGCTGGAGG CAGTGGCCTG CTCCCACCTC
 1651 CACCCGCGCT CTGCGGGGCC TCTGCCTGTG ATGTCTCCGT ACGTGTGGTG
 1701 GTGGGTGAGC CCACCGAGGC CAGGGTGGTT CCGGGCCGGG GCATCTGCCT
 1751 GGACCTCGCC ATCCTGGATA GTGCCTTCCT GCTGTCCCAG GTGGCCCCAT
 1801 CCCTGTTTAT GGGCTCCATT GTCCAGCTCA GCCAGTCTGT CACTGCCTAT
 1851 ATGGTGTCTG CCGCAGGCCT GGGTCTGGTC GCCATTTACT TTGCTACACA
 1901 GGTAGTATTT GACAAGAGCG ACTTGCCAA ATACTCAGCG TAGAAAACTT
 1951 CCAGCACATT GGGGTGGAGG GCCTGCCTCA CTGGGTCCCA GCTCCCCGCT
 2001 CCTGTTAGCC CCATGGGGCT GCCGGGCTGG CCGCCAGTTT CTGTTGCTGC
 2051 CAAAGTAATG TGGCTCTCTG CTGCCACCCT GTGCTGCTGA GGTGCGTAGC
 2101 TGCACAGCTG GGGGCTGGGG CGTCCCTCTC CTCTCTCCCC AGTCTCTAGG
 2151 GCTGCCTGAC TGGAGGCCTT CCAAGGGGGT TTCAGTCTGG ACTTATACAG
 2201 GGAGGCCAGA AGGGCTCCAT GCACTGGAAT GCGGGGACTC TGCAGGTGGA
 2251 TTACCCAGGC TCAGGGTTAA CAGCTAGCCT CCTAGTTGAG ACACACCTAG
 2301 AGAAGGGTTT TTGGGAGCTG AATAAACTCA GTCACCTGGT TTCCCATCTC
 2351 TAAGCCCCTT AACCTGCAGC TTCGTTTAAT GTAGCTCTTG CATGGGAGTT
 2401 TCTAGGATGA AACACTCCTC CATGGGATTT GAACATATGA AAGTTATTTG
 2451 TAGGGGAAGA GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC
 2501 CACAGCACTG TCTTTTTGCT GATCCACCCC CTTCTTACCT TTTATCAGGA
 2551 TGTGGCCTGT TGGTCCTTCT GTTGCCATCA CAGAGACACA GGCATTTAAA
 2601 TATTTAACTT ATTTATTTAA CAAAGTAGAA GGAATCCAT TGCTAGCTTT
 2651 TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA
 2701 GGTCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT
 2751 CTCCTGGGGT CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC
 2801 TACTCATCCC AAATGATAAT TCCAAATGCT GTTACCCAAG GTTAGGGTGT

FIGURE 1 - continued

2851 TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT CTCAACGGCT TCCCTAACCA
2901 CCCCTCTTCT CTTGGCCCAG CCTGGTTCCC CCCACTTCCA CTCCCCTCTA
2951 CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCCAAAAT TTCCCCTACC
3001 CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT
3051 TGGAGCTACT GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTTG
3101 TCCATCTCAG CCCCCAGAGT ATATCTGTGC TTGGGGAATC TCACACAGAA
3151 ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG GAGGTCTTAT CTCTCAGGGG
3201 GGGGTTTAAAG TGCCGTTTGC AATAATGTCG TCTTATTTAT TTAGCGGGGT
3251 GAATATTTTA TACTGTAAGT GAGCAATCAG AGTATAATGT TTATGGTGAC
3301 AAAATTAAAG GCTTTCCTTAT

FIGURE 2

1 MVQRLWVSRL LRHRKAQLLL VNLITFGLEV CLAAGITYVP PLLLEVGVVEE
51 KFMTMVLGIG PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL
101 FLIPRAGWLA GLLCPDPRPL ELALLILGVG LLDFCGQVCF TPLEALLSDL
151 FRDPDHCRQA YSVYAFMISL GGCLGYLLPA IDWDTSALAP YLGTQEECLF
201 GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH CCPCRARLAF
251 RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGEGL
301 YQGVPRAPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG
351 TRAVYLASVA AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA
401 SLYHREKQVF LPKYRGDTGG ASSEDSLMTS FLPGPKPGAP FPNGHVAGAG
451 SGLLPPPPAL CGASACDVSV RVVVGEPTEA RVVPGRGICL DLAILDSAFL
501 LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ VVFDKSDLAK
551 YSA

FIGURE 3

DcSUT2 1 MENGTKELNKPQPPSSAAMQLQTPVQKIPTATWKLVLVAAIAAGVQFGWA 50
PROST03 1MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLA 33
51 LQLSLLTPYVQLLGIPHKWAAIWLCPISGMLVQPIVGYSDHCQSSFG 100
34 AGITYVPPLLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASDHWRGRYG 83
101 RRRPFIASGAGCVAISVILIGFAADISYKAGDDMSKTLKPRAVTVFVIGF 150
84 RRRPFIWALSGLLSLFLIPRAGWLAGLLCPDP....RPLELALLILGV 129
151 WILDVANMLQGPCRALLADLCSGDTRRMRSANAFYSFFMAVGNILGYAA 200
130 GLLDFCGQVCFTPLEALLSDLFR.DPDHCRQAYSVYAFMISLGGCLGYLL 178
201 GSYN.NLYKLFPFSKTHACDLYCANLKSCFIISIALIIITVVALSVVRE 249
179 PAIDWDTSALAPYLGTQEELFGLLTLIIFLTCAATLLVAEEAALGPTEP 228
250 NSGPPDDADAAEPPSSGKIPV..FGELLGALKDL....PRPMLLLLIIVT 293
229 AEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRPRTLRLRFVAE 278
294 CLNWIAWFPFILFDTDWMGREIYGGT.....AGQGKLYDQGVVAGALGL 337
279 LCSWMALMTFTLFYTDVFGELYQGVPRAEPTARRHYDEGVRMGSLGL 328
338 LLNSVVLGLTSIAVEYLVRGVGVVKILWGFVNFILAIGLVMTVVSKVAQ 387
329 FLQCAISLVFSLVMDRLVQRFGTRAV.....YLASVAAFPVAA 366
388 HQREHSANGQLLPPSAGVKAGALSLSILGIPLSITYSIPFALASIYSSG 437
367 GATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRG 416
438 SGAGQGLSLGVLNLAIVVPQMIVSVLAGPFDSLFGGGLNLPFVVGAISSA 487
417 DTGGASSEDLSMTSFLPGPKPGAPFPNGHVAGGSGLLPPPPALCGASAC 466
488 ISGVLAIVLLPKPSKDAASKLSLSGTYH..... 515
467 DVSVRVVVGEPTARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQL 516

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 4

GAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCCTCGGCCAGGATCTGAGT
1 -----+-----+-----+-----+-----+-----+ 60
CTTGGTCGGACGTGCGCGACCGAGGCCACTGTGCGCGCGGAGCCGGTCTAGACTCA

GATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAA
61 -----+-----+-----+-----+-----+-----+ 120
CTACTCTGCACAGGGGTGACTCCACGGGGTGTCTGCTCCACAACCTCGTACCCGACTCTT

GCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCTAGGCAGTTGG
121 -----+-----+-----+-----+-----+-----+ 180
CGACCTGGCCGTGGTTTCCCGACCGTCTTACCCGCGGACCGACTAAGGATCCGTCAACC

CGGCAGCAAGGAGGAGAGGCCGAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGA
181 -----+-----+-----+-----+-----+-----+ 240
GCCGTCGTTCTCTCTCCGGCGTCGAAGACCTCGTCTCGGCTCTGCTTCGTCAAGACCT

GTGCCTGAACGGCCCCCTGAGCCCTACCCGCGCTGGCCCACTATGGTCCAGAGGCTGTGGG
241 -----+-----+-----+-----+-----+-----+ 300
CACGGACTTGCCGGGGGACTCGGGATGGGCGGACCGGGTGATACCAGGTCTCCGACACCC

c M V Q R L W V -

TGAGCCGCTGCTGCGGCACCGGAAAGCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG
301 -----+-----+-----+-----+-----+-----+ 360
ACTCGGCGGACGACGCCGTGGCCTTTTCGGGTCGAGAACGACCAAGTTGGACGATTGGAAC

c S R L L R H R K A Q L L L V N L L T F G -

GCCTGGAGGTGTGTTTGGCCGAGGCATCACCTATGTGCCGCTCTGCTGCTGGAAGTGG
361 -----+-----+-----+-----+-----+-----+ 420
CGGACCTCCACACAAACCGGCGTCCGTAGTGGATACACGGCGGAGACGACGACCTTCACC

c L E V C L A A G I T Y V P P L L L E V G -

GGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCT
421 -----+-----+-----+-----+-----+-----+ 480
CCCATCTCCTCTTCAAGTACTGGTACCACGACCCGTAACCAGGTACGACCCGGACACAGA

c V E E K F M T M V L G I G P V L G L V C -

GTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGC
481 -----+-----+-----+-----+-----+-----+ 540
CACAGGGCGAGGATCCGAGTCCGTACTGGTGACCGCACCTGCGATACCGGCGGCGGCCG

c V P L L G S A S D H W R G R Y G R R R P -

CCTTCATCTGGGCACTGTCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCG
541 -----+-----+-----+-----+-----+-----+ 600
GGAAGTAGACCCGTGACAGGAACCCGTAGGACGACTCGGAGAAAGAGTAGGGTTCCCGGC

c F I W A L S L G I L L S L F L I P R A G -

GCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGCTCATCC
601 -----+-----+-----+-----+-----+-----+ 660
CGACCGATCGTCCCGACGACACGGGCCCTAGGGTCCGGGGACCTCGACCGTGACGAGTAGG

c W L A G L L C P D P R P L E L A L L I L -

TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC
661 -----+-----+-----+-----+-----+-----+ 720
ACCCGACACCCGACGACCTGAAGACACCGGTCCACACGAAGTGAGGTGACCTCCGGGACG

c G V G L L D F C G Q V C F T P L E A L L -

FIGURE 4 – continued

TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCA
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 AGAGACTGGAGAAGGCCCTGGGCCTGGTGACAGCGGTCCGGATGAGACAGATACGGAAGT
 C S D L F R D P D H C R Q A Y S V Y A F M -
 TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTG
 781 -----+-----+-----+-----+-----+-----+-----+ 840
 ACTAGTCAGAACCCCGACGGACCCGATGGAGGACGGACGGTAACCTGACCCTGTGGTCAC
 C I S L G G C L G Y L L P A I D W D T S A -
 CCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCT
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 GGGACCGGGGATGGACCCGTGGGTCTCTCACGGAGAAACCGGACGAGTGGGAGTAGA
 C L A P Y L G T Q E E C L F G L L T L I F -
 TCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGTGGGCCCCACCG
 901 -----+-----+-----+-----+-----+-----+-----+ 960
 AGGAGTGGACGCATCGTCGGTGTGACGACCACCGACTCCTCCGTCGCGACCCGGGGTGGC
 C L T C V A A T L L V A E E A A L G P T E -
 AGCCAGCAGAAGGGCTGTGCGCCCCCTCCTTGTGCCCCACTGCTGTCCATGCCGGGCCC
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 TCGGTCGTCTTCCCACAGCCGGGGGAGGAACAGCGGGGTGACGACAGGTACGGCCCCGG
 C P A E G L S A P S L S P H C C P C R A R -
 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCA
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080
 CGAACCAGAAAGGCCTTGGACCCGCGGGACGAAGGGGCCGACGTGGTCGACACGACGGCGT
 C L A F R N L G A L L P R L H Q L C C R M -
 TGCCCCGACCCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGA
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140
 ACGGGGCGTGGGACGCGGCCGAGAAGCACCAGACTCGACACGTGACCTACCGTGAGTACT
 C P R T L R R L F V A E L C S W M A L M T -
 CCTTCACGCTGTTTTACACGGATTTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCAGAG
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200
 GGAAGTGCACAAAATGTGCCTAAAGCACCCGCTCCCCGACATGGTCCCGCACGGGTCTC
 C F T L F Y T D F V G E G L Y Q G V P R A -
 CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCCGATGGGCAGCCTGG
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 GACTCGGCCCGTGGCTCCGGGCCTCTGTGATACTACTCCGCAAGCCTACCCGTGCGACC
 C E P G T E A R R H Y D E G V R M G S L G -
 GGCTGTTCTGTCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320
 CCGACAAGGACGTACGCGGTAGAGGGACCAGAAGAGAGACCAGTACCTGGCCGACCACG
 C L F L Q C A I S L V F S L V M D R L V Q -
 AGCGATTCCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCTGTGGCTGCCG
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380
 TCGCTAAGCCGTGAGCTCGTCAGATAAACCGGTACACCGTCGAAAGGGACACCGACGGC
 C R F G T R A V Y L A S V A A F P V A A G -

FIGURE 4 - continued

```

GTGCCACATGCCTGTCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGT
1381 -----+-----+-----+-----+-----+-----+ 1440
CACGGTGTAACGGACAGGGTGTACACCCGCACCACTGTGAAGTCGGCGGGAGTGGCCCA
c      A T C L S H S V A V V T A S A A L T G F -
TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGA
1441 -----+-----+-----+-----+-----+-----+ 1500
AGTGAAGAGTCGGGACGTCTAGGACGGGATGTGTGACCGGAGGGAGATGGTGGCCCTCT
c      T F S A L Q I L P Y T L A S L Y H R E K -
AGCAGGTGTTCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC
1501 -----+-----+-----+-----+-----+-----+ 1560
TCGTCCACAAGGACGGGTTTATGGCTCCCTGTGACCTCCACGATCGTCACTCCTGTTCGG
c      Q V F L P K Y R G D T G G A S S E D S L -
TGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGG
1561 -----+-----+-----+-----+-----+-----+ 1620
ACTACTGGTCGAAGGACGTTCCGGGATTTCGGACCTCGAGGGAAGGGATTACCTGTGCACC
c      M T S F L P G P K P G A P F P N G H V G -
GTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGCGGGGCTCTGCCTGTG
1621 -----+-----+-----+-----+-----+-----+ 1680
CACGACCTCCGTACCGGACGAGGGTGGAGGTGGGCGCGAGACGCCCCGAGACGGACAC
c      A G G S G L L P P P P A L C G A S A C D -
ATGTCTCCGTACGTGTGGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCCGGGCGGGG
1681 -----+-----+-----+-----+-----+-----+ 1740
TACAGAGGCATGCACACCACCCACTCGGGTGGCTCCGGTCCCACCAAGGCCCGGGCC
c      V S V R V V V G E P T E A R V V P G R G -
GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCTGCTGTCCCAGGTGGCCCCAT
1741 -----+-----+-----+-----+-----+-----+ 1800
CGTAGACGGACCTGGAGCGGTAGGACCTATCACGGAAGGACGACAGGGTCCACCGGGGTA
c      I C L D L A I L D S A F L L S Q V A P S -
CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTG
1801 -----+-----+-----+-----+-----+-----+ 1860
GGGACAAATACCCGAGGTAAACAGGTGAGTTCGGTCAGACAGTGACGGATATACCACAGAC
c      L F M G S I V Q L S Q S V T A Y M V S A -
CCGAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCG
1861 -----+-----+-----+-----+-----+-----+ 1920
GGCGTCCGGACCCAGACCAGCGGTAAATGAAACGATGTGTCCATCATAAACTGTTCTCGC
c      A G L G L V A I Y F A T Q V V F D K S D -
ACTTGGCCAAATACTCAGCGTAGAAAACCTTCCAGCACATTGGGGTGGAGGGCCTGCCTCA
1921 -----+-----+-----+-----+-----+-----+ 1980
TGAACCGGTTTATGAGTCGCATCTTTTGAAGGTGCTGTAAACCCACCTCCCGGACGGAGT
c      L A K Y S A *
CTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTT
1981 -----+-----+-----+-----+-----+-----+ 2040
GACCCAGGGTCGAGGGGCGAGGACAATCGGGGTACCCCGACGGCCCGACCGGCGGTCAAA

```

FIGURE 4 - continued

2041 CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGC 2100
 -----+-----+-----+-----+-----+-----+-----+
 GACAACGACGGTTTCATTACACCGAGAGACGACGGTGGGACACGACGACTCCACGCATCG
 TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCCCACTCTCTAGGGCTGCCTGAC
 2101 -----+-----+-----+-----+-----+-----+-----+ 2160
 ACGTGTGACCCCCGACCCCGAGGGAGAGGAGAGAGGGGTCAGAGATCCCGACGGACTG
 TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT
 2161 -----+-----+-----+-----+-----+-----+-----+ 2220
 ACCTCCGAAGGTTCCCCCAAAGTCAGACCTGAATATGTCCCTCCGGTCTTCCCCGAGGTA
 GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT
 2221 -----+-----+-----+-----+-----+-----+-----+ 2280
 CGTGACCTTACGCCCCCTGAGACGTCCACCTAATGGGTCCGAGTCCCAATTGTGATCGGA
 CCTAGTTGAGACACACCTAGAGAAGGGTTTTGGGAGCTGAATAAACTCAGTCACCTGGT
 2281 -----+-----+-----+-----+-----+-----+-----+ 2340
 GGATCAACTCTGTGTGGATCTCTTCCCAAAACCCCTCGACTTATTTGAGTCAGTGGACCA
 TTCCCATCTCTAAGCCCCCTAACCTGCAGCTTCGTTTAAATGTAGCTCTTGCATGGGAGTT
 2341 -----+-----+-----+-----+-----+-----+-----+ 2400
 AAGGGTAGAGATTGGGGAATTGGACGTGAAGCAAATTACATCGAGAACGTACCCCTCAA
 TCTAGGATGAAACACTCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGA
 2401 -----+-----+-----+-----+-----+-----+-----+ 2460
 AGATCCTACTTTGTGAGGAGGTACCCCTAACTTGTATACTTTCAATAAACATCCCCTTCT
 GTCTGAGGGGCAACACACAAGAACCAGGTCCCTCAGCCACAGCACTGTCTTTTGTCT
 2461 -----+-----+-----+-----+-----+-----+-----+ 2520
 CAGGACTCCCCGTTGTGTCTTGGTCCAGGGGAGTCGGGTGTCGTGACAGAAAAACGA
 GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCTTCTGTTGCCATCA
 2521 -----+-----+-----+-----+-----+-----+-----+ 2580
 CTAGGTGGGGGAGAATGGAATAAGTCTTACACCGACAACCAGGAAGACAACGGTAGT
 CAGAGACACAGGCATTTAAATATTTAACTTATTTATTTAAACAAAGTAGAAGGGAATCCAT
 2581 -----+-----+-----+-----+-----+-----+-----+ 2640
 GTCTCTGTGTCCGTAATTTATAAATTGAATAAATAAATGTGTTTCATCTTCCCTTAGGTA
 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGTGGGGGATCCCCAACAAATCA
 2641 -----+-----+-----+-----+-----+-----+-----+ 2700
 ACGATCGAAAAGACACAACCACAGATTATAAACCCATCCACCCCCCTAGGGGTGTTAGT
 GGTCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCTCTGCGGT
 2701 -----+-----+-----+-----+-----+-----+-----+ 2760
 CCAGGGGACTCTATCGACCAGTAACCCGACTAGTAACGGTCTTAGAAGAAGAGGACCCCA
 CTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAAATCTACTCATCCCAATGATAAT
 2761 -----+-----+-----+-----+-----+-----+-----+ 2820
 GACCGGGGGGTTTACGGATTGGGTCTGGAACCTTTAAGATGAGTAGGGTTTACTATTA
 TCCAAATGCTGTTACCCAAGGTTAGGGTGTGAAGGAAGGTAGAGGTGGGGCTTCAGGT
 2821 -----+-----+-----+-----+-----+-----+-----+ 2880
 AGGTTTACGACAATGGGTTCGAATCCCACTTCTTCCATCTCCACCCCGAAGTCCA
 CTCAACGGCTTCCCTAACCAACCCCTCTTCTCTTGGCCCCAGCCTGGTTCCCCCACTTCCA
 2881 -----+-----+-----+-----+-----+-----+-----+ 2940
 GAGTTGCCGAAGGGATTGGTGGGGAGAAGAGAACCGGTGCGACCAAGGGGGGTGAAGGT
 CTCCCCCTTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCAAAATTTCCCTTACC
 2941 -----+-----+-----+-----+-----+-----+-----+ 3000
 GAGGGGAGATGAGAGAGATCTGACCCGACTACTTCCGTGACGGGTTTTAAAGGGGATGG

FIGURE 4 - continued

```
CCCAACTTTCCCCTACCCCCAAGTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
3001 -----+-----+-----+-----+-----+-----+ 3060
GGGTTGAAAGGGGATGGGGGTTGAAAGGGGTGGTCGAGGTGTTGGGACAAACCTCGATGA

GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
3061 -----+-----+-----+-----+-----+-----+ 3120
CGTCCTGGTCTTCGTGTTTCACGCCAAAGGGTTCGGAAACAGGTAGAGTCGGGGGTCTCA

ATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCACCCCCTGCCTGAGCTAAGG
3121 -----+-----+-----+-----+-----+-----+ 3180
TATAGACACGAACCCCTTAGAGTGTGTCTTTGAGTCCTCGTGGGGACGGACTCGATTCC

GAGGTCTTATCTCTCAGGGGGGGGTTTAAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
3181 -----+-----+-----+-----+-----+-----+ 3240
CTCCAGAATAGAGAGTCCCCCCCCAAATTCACGGCAAACGTTATTACAGCAGATAAATA

TTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC
3241 -----+-----+-----+-----+-----+-----+ 3300
AATCGCCCCACTTATAAAATATGACATTCAGTTCGTTAGTCTCATATTACAAATACCACTG

AAAATTAAAGGCTTTCTTAT
3301 -----+-----+ 3320
TTTTAATTCCGAAAGAATA
```

Figure 5
Expression of Prost 3 in Human Tissue

